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BD112709 Regularor
AR209012 Sequence
AR260585 Sequence
AR260585 Sequence
BD132698 Regularor
AR209001 Sequence
BD132699 Regularor
AR209002 Sequence
AR209002 Sequence
AR209003 Sequence
AR209003 Sequence
AR271018 Sequence
AR271018 Sequence
AR271018 Sequence
AR275254 Sequence
AR275255 Sequence
AR275255 Sequence
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                                                                                                                                                                                                                                                                                                                                          Unclassified.
1 (Dases 1 to 661)
Fischhoff, D.A., Fuchs, R.L., McPherson, S.A., Lavrik, P.B. and
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Pred. No. 2.5e-163;
0; Mismatches 30; Indels
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Perlak, F.J.
Insect.resistant plants
Jetent: EP 0289479-A2 34 02-NOV-1988;
Location/Qualifiers
1. .661
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                     DNA
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Sequence 34 from Patent BP 0289479.
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CVU10463
CVU10491
CVU10458
CVU10458
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AR482071
BD132700
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AR209001
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BD132699
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Best Local Similarity 94.5
Matches 586; Conservative
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AR229554 Sequence
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AR271019 Sequence
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AR143709 Sequence
AR143713 Sequence
AR143712 Sequence
BD008404 Glyphosat
AR143712 Sequence
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AR143712 Sequence
BD013916 Vermin da
AR003011 Sequence
AX151106 Sequence
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107318 Sequence 30
                                                         ; Search time 7671 Seconds
(without alignments)
4649.073 Million cell updates/sec
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Compugen Ltd.
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        GenCore version (c) 1993 - 2005
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Maximum Match 100%
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Perfect score:
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                                                           380 GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGAGGCC
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                                                                                                                         440 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA
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Pred. No. 2.7e-163;
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Plants and plant cells transformation
AMPA-N-acetyltransferase
Patent: US 6448476-A 29 10-SEP-2002;
Location/Qualifiers
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Sequence 29 from patent US 6448476.
AR229556.1 GI:27269172
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/wol_type="genomic DNA"
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ilarity 94.5%;
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VERSION
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AUTHORS
TITLE
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                                       GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
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1 (bases 1 to 661)
Puche, R.L., Kishore, G.M. and MacIntosh, S.C.
Method for improving the efficacy of insect
Patent: EP 0339009-A2 30 25-OCT-1989;
Location/Qualifiers
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/organism="unknown"
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                                                                                                                              GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAAAGGAAGTTCATTT
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                                                                                                                  GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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Barry,G.F.
Plants and plant cells transformation 1
AMPA.N-acetyltransferase
Patent: US 6448476-A 31 10-SEP-2002,
Location/Qualifiers
                                                                                                                                                                                                                                                     Sequence 31 from patent US 6448476.
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/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                 CATTTGGAGAGGACACGCTG 627
                                                                                                                                                                    CATTTGGAGAGGACACGCTG 731
                                                                                                                                                                                                                                                                                                AR229557.1 GI:27269173
                                                                                                                                                                                                                                                                                                                                                  Unclassified.
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                                                GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAAAGGAAGTTCATTT
GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
              GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                                                                                                      GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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Plants and plant cells transformation to a Plants and plant cells transformation to a AMPA-N-acetyltransferase
Patent: US 6448476-A 25 10-SEP-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                         Sequence 25 from patent US 6448476.
AR229554
AR229554.1 GI:27269170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
/wol_type="genomic DNA'
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Unclassified.
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508 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567 652 GATGACGCACAATCCTACCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711 568 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627 712 CATTTGGAGAGGACACGCTG 731 628 CATTTGGAGAGACACCTG 647	AR271019	116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGC 175 	176 CAGCTATCTGTCATCATCAAAAGGACAGTAGAAAAGGAAGG	236 ATCATTGCGATAAAGAAAGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295	296 ATGGACCCCCACCACGAGGATCGTGGAAAAAGAGACGTTCCAACCACGTCTTCAA 355 	356 AGCAAGTGGATTGATGTGATTGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA 411	412 AACCTCCTGGATTCCATTGCCCAGCTATCTGTCACTCATCAAAAGGACAGTAGAAAAG 471	472 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531 	532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACGAGGAGGATCGTGGAAAAGAA 591 	592 GACGTICCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651	652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAAAGGAAGTTCATTT 711
8 6 6 8	RESULT AR27101 COORD DECTNIT ACCESSI VERSION KEYWORE ORGAN REFEREN ACATHO TITLE JOURN FEATURE SO ORIGIN ORIGIN QUEET BEST	oy D	Qy Db	\$ B	S S	yo g	Qy	λ α	δ ν	S G	ò
448 TCTGCCGACAGTGGTCCCAAA 592 GACGTTCCAACCAGTCTTCA 508 GACGTTCCAACCAGTCTTCA 652 GATGACGCACATCCACTAT 568 GATGACGCACAATCCCACTAT 568 GATGACGCACAATCCCACTAT		Ouery Match 75.3%; Score 554; DB 6; Length 3469; Best Local Similarity 94.5%; Pred. No. 2.7e-163; Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;	Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175 Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 87	OY 176 CAGCTATCTGTCATCAAAAGACAGTAGAAAAGGAAGGTGGCACGTACAAATGCC 235	OY 236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295	OY 296 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355	Oy 356 AGCAAGTGGATTGATGTGATTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411 Db 268 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAGGGTAATATCCGGA 327	OY 412 AACCTCCTGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471	Qy 472 GAAGGIGGCACCTACAAAIGCCATCATIGCGATAAAGGAAAGG	Qy 532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACGAGGAGCATCGTGGAAAAAGAA 591 Db 448 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA 507	Oy 592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651

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E 1 (bases I to 8012)

E 2 (bases I to 8012)

E 3 (Alphosate resistant transgenic plants

G 1yphosate resistant transgenic plants

G 1yphosate resistant transgenic plants

D 2001503280-A 1 13-MAR-2001;

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                                                                                                                 DNA
plants.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                              Glyphosate resistant transgenic : BD008400
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3644 CATTTGGAGAGGACACGCTG 3663
                                                                                                                                                                                 BD008400.1 GI:18636773
JP 2001503280-A/1.
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Best Local Similarity
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568 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627
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Mannerloef, M., Tenning, P.Peter. and Steen, P.
Transgenic plants
Patent: US 6204436-A 1 20-MAR-2001;
Location/Qualifiers
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                                 2347 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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/organism="unknown"
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                  GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATTCCTCCCACTGACGTAAAG
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                                                        GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAAGGAAGTTCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.3%; Score 554; DB 6; Length 83
Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels
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Corbin,D.R. and Romano,C.P.
Wethods for transforming plants to express Cry2Ab
.delta.-endotoxins targeted to the plastids
Patent: US 6489542-A 16 03-DEC-2002;
                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                            8349 bp
Sequence 16 from patent US 6489542.
AR260588
AR260588.1 GI:27311143
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                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .8349
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                                                                                                                CATTTGGAGAGACACGCTG
                                                                                                                                                                                                                                                                                                                      Unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 8798)

Mannerloef, M., Tenning, P.Peter. and Steen, P.
Transgenic plants

Patent: US 6204436-A 4 20-MAR-2001;

Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 4 from patent US 6204436.
AR143712. GI:15104998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3023 TCCGATGTGAGACTTTTCAACAAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 3082
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Pred. No. 2.8e-163;
0; Mismatches 30; Indels
                                                                                                                                                                                    linear
                                                                                                                                                                                                                                             BD008404.1 GI:18636777
JP 2001503280-A/5.
unidentified
unidentified
unclassified.
1 (bases 1 to 8418)
Mannerloef,M., Tenning,P.P. and Steen,P.
Glyphosate resistant transgenic plants
Patent: JP 2001503280-A 5 13-MAR-2001;
                                                                                                                                                                   BD008404 8418 bp DNA
Glyphosate resistant transgenic plants.
BD008404

    .8418
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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                                               3623 CATTTGGAGAGGACACGCTG 3642
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94.5%;
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Best Local Similarity 94.5
Matches 586; Conservative
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OS Unidentified
PN JP 2001112490-A/19
PP 24-APR-2001
PP 07-SEP-2000 UP 2000272128
PR 29-APR-1997 US
PY C12M15/09, AD1195/00, C7X14/325, C12N5/10/(C12N1/21, C12P21/02, PC (C12N15/09, C12R1:07), C12N15/00, C12N15/00, C12R1:07), CC
Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC Vermin damage-resistant plant
FH Key
Location/C
FT Source
                                            3493 GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGACGC 3552
                                                                                                                                                                                                                                                                          3732
                                                                                                               3553 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAA 3612
                                                                                                                                                                                         3613 GACGTTCCAACCACCACGTTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 3672
                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 27-AUG-2002
                                                                                                                                                                  651
                                                                                                                                                                                                                                       711
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                                                                                                                                                                                                                                                      3673 GAIGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAAAGGAAGTTCATTT
                                                                                                                                                                  592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                                                                                                                                                                                       652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 TCCGATGTGGAGACTTTTCAACAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.1%; Score 552.4; DB 6; ilarity 94.4%; Pred. No. 8e-163; Conservative 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unclassified.
1 (bases 1 to 661)
Fiskehof,D.A., Fuchs,R.L., Labrik,P.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                BD013916 661 bp
Vermin damage-resistant plant.
BD013916
BD013916 GI:22554245
JP 2001112490-A/19.
unidentified
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                                                                          3673 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 3732
                                                                                                                                                                                                                                                        PAT 31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aregacececacecaceaegagearegregaaaaaagaagacerrecaaegecrererreaa 3372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAAGGACGTTCCAACCACGTCTTCAA 355
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ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCCAAAG
                                                       GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAAAGGAAGTTCATTT
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Pred. No. 2.8e-163;
0; Mismatches 30; Indels
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31-0CT-1997 US 60/112003
MARIE MANNERLOEF, PAUL PETER TENNING, PER STEEN
                                                                                                                                                                                                                                                         linear

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/organism='Unidentified'

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Mannerloef M., Tenning, P.P. and Steen, P.
Glyphosate resistant transgenic plants
Patent: JP 2001503280-A 4 13-MAR-2001;
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                                                                                                                                                                                                                                                Glyphosate resistant transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .8798
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OS Unidentified
PN JP 2001503280-A/4
PP 13-MAR-2001
PF 29-OCT-1998 JP 1999525342
PR 31-OCT-1997 US 60/1120
PI MARIE MANNERACEF, PAUL PET C12N15/82, A0145/00, A0145/10
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location//
FT Source /organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                             3733 CATTTGGAGAGACACGCTG 3752
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JP 2001503280-A/4.
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llarity 94.5%;
Conservative
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Best Local 8
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                                                                                                                                                                                                                                                                      DEFINITION
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TITLE
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320 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAAGATAGTGGAAAAA 379
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                                                                                                                                                                               AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
                                                                                                                             TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAA 591
                                                                                                                                                       GACGITCCAACCACGICITCAAAGCAAGIGGAIIGAIGIGAIAICTCCCACIGACGIAAGG 651
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Aav63741 Plasmid p Aad01286 Rice tran Aad01286 Rice tran Aad15563 pM0N33828 Aaa15562 pM0N33829 Aaa15564 pM0N33829 Aaa15562 pM0N33829 Aaa1562 pM0N33829 Aaa1562 pM0N33829 Aaa1562 pM0N33829 Aaa7623 Vector pl Aav63723 Vector pl Aav63724 Vector pl Aax51641 Bacillus Aax51641 Bacillus Aas17547 Plasmid p Aas17547 Plasmid p Aas17547 Plasmid p Aas175876 Luciferas Abv75876 Luciferas Abv75876 Luciferas Aac66931 Plant sig

Title: Perfect score:

Sequence:

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Scoring table:

Searched:

Minimum DB Maximum DB

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New bi-directional promoter complex comprising a modified enhancer region including at least 2 enhancer sequences, and at least 2 core promoters, useful for enhancing or improving transcriptional activity of transgenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a bi-directional promoter complex comprising a modified enhancer region that includes at least 2 enhancer sequences, and
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ABX95185
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Add1790 Bt.ory3Bb
Abx95186 B. thurin
Adx98498 B. thuring
Adx98490 B. thuring
Aax57305 Sugar bee
Aax1555 pMON30464
Aax57309 Sugar bee
Aax57308 Sugar bee
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Abx95190 B. thurin
Aaz51642 Bacillus
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Compugen Ltd.
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AAD01017
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AAD61794
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ABX95190
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Result No.

expression related bidirectional dual promoter complex

(first entry)

29-NOV-2002

dual promoter complex; transcription; transgene;

agronomic performance; transformation; ds

Bidirectional

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modified enhancer region in a divergent orientation. The bi-directional promoter complex is useful for enhancing transcriptional activity of transgenes to improve agronomic performance used in genetic transformation with plants. Vectors that include the bi-directional promoter complex may be used to express foreign genes in mammalian cells and in plant cells including dicots and monocots. This sequence represents a bidirectional dual promoter complex useful for enhancing transcriptional activity of transgenes
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                                                                                                                                                  Sequence 736 BP; 222 A; 176 C; 175 G; 163 T; 0 U; 0 Other;
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                                                                                                                                                                            Score 734.4; DB 6;
Pred. No. 6.9e-232;
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Best Local Similarity 99.9
Matches 735; Conservative
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ABS53105 standard; DNA; 1360 BP.

ABS53105 ID ABS5 XX

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a bi-directional promoter complex comprising a modified enhancer region that includes at least 2 enhancer sequences, an at least 2 core promoters. The core promoters are on either side of the modified enhancer region in advergence or orientation. The bi-directional promoter complex is useful for enhancing transcriptional activity of transgenes to improve agronomic performance used in genetic transformation with plants. Vectors that include the bi-directional promoter complex may be used to express foreign genes in mammalian cells and in plant cells including dicots and monocots. This sequence represents a bidirectional dual promoter complex useful for enhancing
                                                                                                                                                                                                           complement of this sequence is also claimed as SEQ ID number 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTC
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in claim 10 a
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                                                                                                                                                                                                                                                                                                                                                                                                          Gray DJ;
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Query Match
Best Local Similarity
Matches 586; Conserv
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                      TCTTCAAAGCAAGTGGATTGATGTGATTGCAGTGAGACTTTTCAACAAAGGGTAATATCG 1061
                                             528
                                                                          GAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTA 648
                                                                                                                                              707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A fragment of the CaMV35S promoter (-343 to +9), previously constructed by Odell et al. (1985) Nature 313:810-812, is necessary for maximal expression of the promoter. It was exiced as a ClaI-HindIII fragment, made blunt ended with DNA pol I and inserted into the HincII site of
                                                     AAGGAAGGTGGCACCTACAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGAT
                                                                                                                                                                                                                                                     Bacillus thuringiensis var. tenebrionis toxin gene, enhanced promoter;
CaMV35S; pMON893; Coleopteran insects; transformed plants;
                                           AAGGAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGAT
                                                                                                                                                                                                                                       Enhanced CaMV35S promoter used in pMON893 B.thuringiensis toxin prodn
                                                                                                                                      AGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetically transformed plants with toxicity to Coleopteran insects obtd. using chimeric gene contg. sequence encoding toxin protein of Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perlak
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lavrik PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mcpherson SA,
                                                                                                                                                                                                                                                                                                                       /number= 1
/note= "duplicated e
289. .541
/*tag= b
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       /number= 2
/note= "duplicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page ?; 52pp; English.
                                                                                                                                                                                          BP
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                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fuchs RL,
                                                                                                                                                                                          AAN81003 standard; DNA;
                                                                                                                                                                                                                                                                                                           /..../
/*tag=
                                                                                                                                                                                                                                                                                    Bacillus thuringiensis.
                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1988-309416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (MONS ) MONSANTO CO
                                                                                                                                                                                                                                                                      chimaeric gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fischhoff DA,
                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                           29-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                             EP289479-A.
1002
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                                                           1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711
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                                                                                                                                                                                                                                                                                                                                                                                                                   295
                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559
                                                                                                                                                                                                                                                                                          79
                     into the
promoter
AAN81000-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG
                                                                                                                                                                                                                                                                               ATCATTGCGATAAAGGAAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 GAAGGTGCTTCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                                                                                                                                                                                                                                     ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u> aecaagregarrigargregargregargregaetrrrreaeaaaggraararecega</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                                                                                                                                                                                                   TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAAAAGAAGACGTTCCAACCACGTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter; Bacillus thuringiensis; toxin protein; insecticide; pMON893.
                                                                                                                                                                                                            Gaps
      this
into
                                                                                                                                                                                                               4 ;
pUC18. The upstream region of the 35S promoter was exiced from plasmid as a HindIII-ECORV fragment (-343 to -90) and inserted saame plasmid between the HindIII and PBII sites. The enhanced thus contains a duplication of sequences -343 to -90. See also
                                                                                                                                                                      Length 661;
                                                                                                                             Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enhanced CaMV35S promoter used in plasmid pMON893
                                                                                                                                                                 Score 554; DB 1; L
Pred. No. 2.9e-172;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATTTGGAGAGACACGCTG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATTTGGAGAGGACACGCTG
                                                                                                                                                                 75.3%;
94.5%;
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                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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us-10-075-105c-1.rng

619

651

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440 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphonate herbicide tolerance, aminomethyl phosphonic acid, AMPA, AAT, acyltransferase; transacylase; recombinant plant; expression cassette; corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide; CTP; glyphosate oxidase; GOX; glyphosate oxidoreductase; phnO gene; self-fertilisation; hetero-fertilisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acyltransferase (AAT) enzyme"
/function= "Transfers acyl group from an acylcarrier
(CoA) to the free amino group of aminomethylphosphonate"
                                                                                                                                                                                                                                                                                                                                                                                                                      Expression cassette-4 comprising modified E. coli P2A phnO coding gene.
                                   592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                                                           652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                                560 GATGACGCACAATCCCACTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '*tag= a
'note= "Plant functional heterologous promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/product=_"Escherichia coli modified P2A AMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/note= "Enhances expression of the phnO gene"
149. .1426
/*tag= d
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/note= "Enhances expression of the phnO gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                 731
                                                                                                                                                                                                                  620 CATTTGGAGAGACACGCTG 639
                                                                                                                                                                                                                                                                                                            AAD01017 standard; DNA; 2107 BP.
                                                                                                                                                                                 CATTTGGAGAGGACACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US027152
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .685
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P-PSDB; AAY71251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transit peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                               712
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                                                                                                                                                                                                                                                                                                                                              AAD01017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'UTR
                                                                                                                                                                                                                                                                      AAD01017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A fragment of the CaMV35S promoter (-343 to +9) in pUC13 was excised as a ClaI-HindIII fragment and blunt-ended. This was inserted into the HinCII site of pUC18. The upstream region of the 3SS promoter was excised as a HindIII-ECORV fragment (extending from -143 to -90) and inserted into the same plasmid between the HindIII and PstI sites. The enhanced promoter thus contains a duplication of sequences between -343 ans -90. The promoter is used in plasmid pMON893 to express Bacillus thuringiensis toxin with a potentiating amt. Of a trypsin inhibitor. This is useful as an insecticide. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                   Toxin protein of Bacillus thuringiensis bacteria - improved in efficacy using a potentiating amt. of a trypsin inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGGAGCATCGTGGAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGAIGCCTCTGCCGACAGTGCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 554; DB 1; Length 661;
Pred. No. 2.9e-172;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;
                                   /*tag= a
/note=_"duplicated enhancer sequence"
                                                                                       /*tag= b
/note= "duplicated enhancer sequence"
                                                                                                                                                                                                                                                                                                                             SC;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 14; 56pp; English.
                                                                                                                                                                                                                                                                                                                             Macintosh
                                                                                                                                                                                                                   89EP-00870047
                                                                                                                                                                                                                                                     88US-00179709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.3%;
llarity 94.5%;
Conservative
                                                                    .541
                                                                                                                                                                                                                                                                                                                             Kishore GM,
                                                                                                                                                                                                                                                                                        (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1989-311431/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 586; Conserv
                 misc_feature
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                                                                                                                                                                                                                   14-APR-1989;
                                                                                                                                                                                                                                                     11-APR-1988;
                                                                                                                                            EP339009-A.
                                                                                                                                                                                                                                                                                                                             Fuchs RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
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The patent discloses a method for selectively enhancing the phosphonate and rice plants, by transforming the plants with an expression cassette. It comprises of a structural DNA sequence, that encodes an aminomethyl phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of Nacylation of AMPA. This sequence has an amino terminal chloroplast transit peptide (CTP), that targets AAT to the chloroplast Co-expression of glyphosate oxidase (GOX) gene, encoding glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase, along with AAT provides the transformed plants with higher resistance to phosphonate herbicides. This method is useful for enhancing phosphonate herbicides such as glyphosate and AMPA tolerance, in recombinant plants and to prevent self-fettilisation and enhance hetero-fertilisation. The
                                                                                                                                                                                                                                                                                                                                  present DNA sequence is the expression cassette-4, comprising a plant operable promoter and 5' sequences like, 5' untranslated region (UTR) and intron, linked to modified E coli phnO coding region encoding P2A AMPA acyltransferase (AAT) enzyme and plant operable termination sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACGAGGAGGAGCATCGTGGAAAAAGAA 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAG 471
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cotton, canola and rice plants involves transforming plants with phosphonate metabolizing genes encoding acyltransferase enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.3%; Score 554; DB 3; Length 2107; 94.5%; Pred. No. 5.1e-172; ive 0; Mismatches 30; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2107 BP; 497 A; 531 C; 551 G; 528 T; 0 U; 0 Other;
                                                      Disclosure; Page 170-172; 179pp; English.
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586; Conservative
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The patent discloses a method for selectively enhancing the phosphonate herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola and rice plants, by transforming the plants with an expression cassette. It comprises of a structural DNA sequence, that encodes an aminomethyl phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of N-acylation of AMPA. This sequence has an amino terminal chloroplast transit peptide (CTP), that targets AAT to the chloroplast. Co-expression of glyphosate oxidase (GCX) gene, encoding glyphosate oxidoreductase, along with AAT provides the transformed plants with higher resistance to phosphonate herbicides. This method is useful for enhancing phosphonate
                                                                                                                                                   acylransferase; transacylase; recombinant plant; expression cassette; corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide; CTP; glyphosate oxidase; GOX; glyphosate oxidase; GOX; glyphosate oxidase; phnO gene; self-fertilisation; hetero-fertilisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function= "Transfers acyl group from an acylcarrier
(CoA) to the free amino group of aminomethylphosphonate"
1849. ,2082
                                                                                                                                      aminomethyl phosphonic acid; AMPA; AAT;
                                                                                                        Expression cassette-2 comprising modified E. coli P2A phnO coding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat, cotton, canola and rice plants involves transforming plants with phosphonate metabolizing genes encoding acyltransferase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= d/note= "Targets the protein to an intracellular organelle, like chloroplast"
                                                                                                                                                                                                                                                                                                                          note= "Plant functional heterologous promoter"
545. .715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= e
/product= "Escherichia coli modified P2A AMPA
                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "Enhances expression of the phnO gene"
                                                                                                                                                                                                                                                                                                                                                                                                          *tag= c
/note= "Enhances expression of the phnO gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acyltransferase (AAT) enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 164-166; 179pp; English.
                                                                                                                                                                                                                                                                               Location/Qualifiers
6. .620
                                                                                                                                      herbicide tolerance;
             BP.
             AAD01015 standard; DNA; 2122
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P-PSDB; AAY71251.
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                                                                                                                                      Phosphonate
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              Escherichia
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                        Synthetic
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herbicides such as glyphosate and AMPA tolerance, in recombinant plants and to prevent self-fertilisation and enhance hetero-fertilisation. The present DNA sequence is the expression cassette-2, comprising a plant operable promoter and 5' sequences like, 5' untranslated region (UTR) and intron, linked to modified E. coli phno coding region encoding P2A AMPA acyltransferase (AAT) enzyme and plant operable termination sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphonate herbicide tolerance, aminomethyl phosphonic acid, AMPA, AAT, acyltransferase; transacylase; recombinant plant; expression cassette; corn; tobacco; wheat; cotton; cannola; rice; chloroplast transit peptide; CTP; glyphosate oxidase; GDX; glyphosate oxidase; GDX; glyphosate oxidoreductase; phnO gene; self-fertilisation; hetero-fertilisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression cassette-5 comprising modified E. coli P2A phnO coding gene.
                                                                                                                                          116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                    GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                                                       ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                  AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
                                                                                               75.3%; Score 554; DB 3; Length 2122; llarity 94.5%; Pred. No. 5.1e-172; Conservative 0; Mismatches 30; Indels
                                                                           Seguence 2122 BP; 495 A; 537 C; 561 G; 529 T; 0 U; 0 Other;
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586; Conserv
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The patent discloses a method for selectively enhancing the phosphonate herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola and rice plants, by transforming the plants with an expression cassette. It comprises of a structural DNA sequence, that encodes an aminomethyl phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of Nacylation of AMPA. This sequence has an amino terminal chloroplast transit peptide (GTP), that targets AAT to the chloroplast. Co-expression of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase, along with AAT provides the transformed plants with higher resistance to phosphonate herbicides. This method is useful for enhancing phosphonate herbicides such as glyphosate and AMPA tolerance, in recombinant plants and to prevent self-fertilisation and enhance hetero-fertilisation. The operable promoter and 5' sequences like intron, linked to modified E. Coli photo coding region, encoding PPA AMPA acyltransferase (AAT) enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Bscherichia coli modified P2A AMPA acyltransferase (AAT) enzyme" /function= "Transfers acyl group from an acylcarrier (CoA) to the free amino group of aminomethylphosphonate" 2172. .2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat, cotton, canola and rice plants involves transforming plants with phosphonate metabolizing genes encoding acyltransferase enzyme.
                                                                                                                                                                                                                                                                                                                                                           /note= "Targets the protein to an intracellular organelle, like chloroplast" 1726. 2160 /*tag= d
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                                                                                                                                                               /*tag= a
/note= "Plant functional heterologous promoter"
670. .1473
                                                                                                                                                                                                                                                    *tag= b
note= "Enhances expression of the phnO gene"
[498. .1725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 173-175; 179pp; English.
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Matches 586; Conserv
coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is an expression cassette from a Cry3Bb plant expression vector pMON3748. It comprises an enhanced Cauliflower mosaic virus (CaMV) 35S promoter sequence, a wheat chlorophyll A/B binding protein untranslated leader sequence, a rice actin intron sequence, a Bacillus thuringiensis delte-endotoxin Cry3Bb variant 11231mv2 coding sequence and a wheat heat shock Hsp17 transcription termination and polyademylation sequence. This expression cassette is used to improve expression of Cry3B variant protein in transgenic plants e.g. maize, to increase insecticidal activity against Coleopteran pests. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207
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                                                                                                                                                  /note= "Wheat heat shock Hsp17 transcription termination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel expression cassettes which express Bacillus thuringiensis Cry3 delta-endotoxin portion which is toxic to coleopteran insect pests, useful for producing transgenic plants with improved insecticidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ;
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          note= "Rice actin intron sequence"
                                                                     11231mv2"
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                                                                                                                                                                        and polyadenylation sequence
                                                                  "Cry3Bb variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 149-152; 171pp; English.
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/label= T-Ta.hsp17
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/product= "C1
3217. .3450
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Matches 586; Conservative
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                                                                                          terminator
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                                                                                        ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA
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//abel= P-CaMV.35S
664...734
//abel= L-Ta.hcbl
/note= "Wheat chlorophyll A/B binding protein
untranslated leader sequence"
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(first entry)
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Bacillus thu
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B. thuringiensis delta endotoxin Cry3Bbl 11231mv2 expression cassette #2.
                                                                                                         The invention relates to novel transgenic plants comprising Bacillus thuringiensis Cry3-delta-endotoxin gene or its variants having coleopteran inhibitory activity. The invention is useful for controlling Coleopteran insect infestation in a field of crop plants. The present sequence is B. thuringiensis Cry3Bb-delta- endotoxin variant expression vector DNA
                 comprises Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 Arcarrecearaaaggaaageccarecregaagarecerereceacaeregereceaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 AGCAAGTGGATTGATGTGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
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                                                                                                                                                                                                                                                                                                                                                                                           116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 iccaigigadactiticaacaagggiaatatccggaacciccicggatccatigcc
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                          Length 3469;
                                                                                                                                                                                                                                                               Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                Indels
                   transgenic plant resistant to Coleopteran pests,
                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                 tch
al Similarity 94.5%; Pred. No. 6.5e-172;
586; Conservative 0; Mismatches 30:
                                      thuringiensis Cry3-delta-endotoxin gene
                                                                             Claim 16; Page 77-80; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                     567
                                      447
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                                                                                                                                                                                                                                              711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic plant, Cry3Bb-delta-endotoxin; Coleopteran pest resistance; insecticide; variant; cyclic; circular; chimeric; rice; wheat; gene; ds.
                                                                                                    GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                      GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
                                                                                                                                                                                                     GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTCATGTGATATCTCCACTGACGTAAGG
                                                                                                                                                                                                                                              GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
                                                                             TCTGCCGACAGTGGTCCCAAAGATGGACCCCCCACCCACGAGGAGCATCGTGGAAAAAGAA
                                                                                                                                                              GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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/note= "Cauliflower mosaic virus 35S promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664. .734
/*tag= b
/note= "Wheat chlorophyll A/B binding protein
uranslated leader sequence (L-Ta.hcbl)"
748. .1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "Rice actin intron (I-Os.Act1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .cry3Bb.11231mv2 expression vector DNA, pMON33748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Bt.cry3Bb.11231mv2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Cauliflower mosaic virus.
Chimeric - Oryza sativa.
Chimeric - Bacillus thuringiensis.
Chimeric - Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       CATTTGGAGAGGACACGCTG 647
                                                                                                                                                                                                                                                                                                                               CATTIGGAGAGGACACGCTG 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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/note= "Wheat h
and polyadenyla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD61794 standard; DNA; 3469
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/*tag= d
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3217. .3420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CaMV.35S) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .640
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P-PSDB; ABW01055.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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                                    388
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The invention relates to a modified polynuclectide which encodes an insecticidal crystal 3 (Cry3) Bacillus thuringiensis delta-endotoxin such as CryBb. The modified polynuclectide is useful for producing a transformed cell, by introducing the modified polynuclectide into a cell such as a plant cell (preferably a maize cell) or a microbial cell. The modified polynuclectide is useful for producing a transformed maize plant cell and regenerating a maize plant cell. by introducing the modified polynuclectide into a maize plant cell. Crom the transformed maize plant cell. A transgenic plant expressing the modified polynuclectide is useful for controlling coleopteran insect infestation in a field of crop plants. The modified polynuclectide is useful for producing transgenic plants expressing higher levels of the insect controlling B. thuringiensis delta-endotoxin. The modified polynuclectide provides up to 10 fold higher levels of insect controlling compositions. In particular, transgenic maize expressing higher levels of the Cry3Bb protein designed to exhibit increased toxicity toward to compositions. In particular, transgenic maize expressing higher levels of the Cry3Bb protein designed to exhibit increased toxicity toward compositions are resistant to the insecticidally active protein. Improved control of
               Cry3Bb1 11231mv2, gene, delta-endotoxin; plant, transgenic; insecticide, crystal 3; Cry3; Coleopteran insect infestation; increased toxicity; ds; season long protection; beetle; maize; rice; expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         te= "Wheat heat shock HSP17 transcription terminator polyadenylation sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for controlling Coleopteran insect
nts encodes insecticidal crystal 3
                                                                                                                                                                                                                                                                                    /noie= "Wheat chlorophyll A/B binding protein untranslated leader sequence"
                                                                                                                                                                                                                                                                                                                                                                       'cons splice= (5'site:NO,3'site:NO)
'note= "Rice actin intron"
                                                                                                                                                                                                                     '*tag≃ a
'note= "Enhanced CW35S promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Cry3Bbl 11231mv2"
3217. .3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Col 141-148; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified polynucleotide useful for on infestation in a field of crop plants en Bacillus thuringiensis delta-endotoxin.
                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLC.
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/note= "Wheat h
and polyadenyla
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                                                                                                                                                                                                                                                                                                                                                                                                            241. .3202
                                                                                                                                                                                                                                                      . 734
                                                                                                                  Oryza sativa.
Cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                                                            number=
                                                                                                                                                                                                                                                                        tag= b
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                                                                                 Bacillus thuringiensis
                                                                                                                                                                                                                                                        664.
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P-PSDB; ABU09202.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_signal
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                                                                                                                                                   Synthetic
                                                                                                    mays
                                                                                                                                                                                                       promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327
susceptible target insect pests and season long protection from insect pathogens is achieved using the modified polynucleotide. The modified polynucleotide reduces the number of transgenic events that have to be screened in order to identify one which contains beneficial levels of one or more insect controlling compositions. The present sequence represents Bacillus thuringiensis delta endotoxin Cry3Bbl 11231mv2 expression cassette #2 DNA
                                                                                                                                                                                                                                                                                                                                                       Arcatrigcgaraaaggaaaaggccarcgrigaagargccrcrgccgacagrggrcccaaag 207
                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                                                                                                                                       rcceargreagacriticaacaaagggraararccggaaaccrccrcggarrccarrgcc
                                                                                                                                                                                                                                                                                                                                                                                                          TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA
                                                                                                                                                                                                          TCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                GAAGGTGCTCTACAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rcrecceacagregreccaaagarggacceccaccagaggaggaggarggagaaaaaaa
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                                                                                                                                                                                                                                                                   CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAAGGTGGCACCTACAAATGCC
                                                                                                                                                                                                                                                                                                                               ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                      ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAAAAGAAGACGTTCCAACCACGTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAAGTGGATTGATGTGAT.....TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis Cry3Bb variant v11231 expression cassette-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delta-endotoxin, Cry3B; Bt toxin, crystal protein; insect pest; insecticide; Coleopteran; expression cassette; transgenic plant; Cry3Bb variant v11231; ds.
                                                                                                                                                                              4,
                                                                                                                                                Length 3469;
                                                                                                                   756 T; 0 U; 0 Other;
                                                                                                                                                                              Indels
                                                                                                                                             Score 554; DB 10;
Pred. No. 6.5e-172;
0; Mismatches 30;
                                                                                                                     ö
                                                                                                                   C; 845
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                                                                                                                   Sequence 3469 BP; 790 A; 1078
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Best Local Similarity 94.5%;
Matches 586; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plant, Cry3Bb-delta-endotoxin, Coleopteran pest resistance, insecticide, variant, cyclic, circular, chimeric, maize, gene, ds.
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                                                                                                      AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA
                                                                                                                                   AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
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/note= "Cauliflower mosaic virus 35S promoter
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3475. .3730
/*tag= d
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Bacillus thuringiensis.
Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Cauliflower mosaic virus.
Chimeric - Zea mays.
Chimeric - Bacillus thuringiensis.
Chimeric - Agrobacterium tumefaciens
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1490. .3451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is an expression cassette from a Cry3Bb plant expression vector pMON33710. It comprises an enhanced Cauliflower mosaic virus (CaMV) 355 promoter sequence, a maize Hsp70 intron sequence, a Bacillus thuringiensis delta-endotoxin Cry3Bb variant AAV11231 coding sequence and a nopaline synthase transcription termination and polyadenylation sequence. This expression cassette is used to improve expression of Cry3B variant protein in transgenic plants e.g. maize, to increase insecticidal activity against Coleopteran pests. (Updated on 15-5EP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                /note= "Agrobacterium tumefaciens nopaline synthase 3' transcription termination and polyadenylation sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel expression cassettes which express Bacillus thuringiensis Cry3 delta-endotoxin portion which is toxic to coleopteran insect pests, useful for producing transgenic plants with improved insecticidal
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//label= 1-2m.Hsp70
/note= "Zea mays Hsp70 intron sequence"
1490. .3451
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Similarity 94.5%; Pred. No. 6.7e-172;
86; Conservative 0; Mismatches 30;
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/label= CaMV35S_promoter
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Agrobacterium tumefaciens.
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Cauliflower mosaic virus.
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                                                                                                                                                                                                                          The invention relates to novel transgenic plants comprising Bacillus thuringiensis Cry3-delta-endotoxin gene or its variants having coleopteran inhibitory activity. The invention is useful for controlling Coleopteran insect infestation in a field of crop plants. The present sequence is B. thuringiensis Cry3Bb-delta- endotoxin variant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                         New transgenic plant resistant to Coleopteran pests, comprises Bacillus
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                                                                                                                                                                                                                                                                                                                                                         Score 554; DB 10;
Pred. No. 6.7e-172;
0; Mismatches 30;
                                                                                                                                                                      thuringiensis Cry3-delta-endotoxin gene
                                                                                                                                                                                                  Claim 16; Page 57-60; Opp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTTGGAGAGGACACGCTG 731
29-AUG-2002; 2002US-00232665
                            99US-00377466.
                                                                                                                                                                                                                                                                                                                                                          75.3%;
94.5%;
                                                                                                                                                                                                                                                                                                                                                                                      Matches 586; Conservative
                                                                                                              2003-810928/76.
                                                     (ROMA/) ROMANO C P.
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                            WPI; 2003-810928/
P-PSDB; ABW01053.
                            19-AUG-1999;
                                                                                                                                                                                                                                                                                                   vector DNA
                                                                                   Romano CP;
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The invention relates to a modified polynucleotide which encodes an insecticidal crystal 3 (Cry3) Bacillus thuringlensis delta-endotoxin such as CryBb. The modified polynucleotide is useful for producing a transformed cell, by introducing the modified polynucleotide into a cell such as a plant cell (preferably a maize cell) or a microbial cell. The modified polynucleotide is useful for producing a transformed maize plant by introducing the modified polynucleotide into a maize plant cell. by introducing the modified polynucleotide into a maize plant cell, by introducing a transformed maize plant cell and regenerating a maize plant from the transformed maize plant cell. A transgenic plant expressing the modified polynucleotide is useful for controlling Coleopteran insect infestation in a field of crop plants expressing higher levels of the insect controlling B. thuringlensis delta-endotoxin. The modified polynucleotide provides up to 10 fold higher levels of insect controlling
                                                                                                                              Cry3Bbv11231, ds, gene, delta-endotoxin, plant, transgenic, insecticide, crystal 3, Cry3, Coleopteran insect infestation, increased toxicity, season long protection; beetle, maize, expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Agrobacterium tumefaciens nopaline synthase transcription terminator and polyadenylation sequence"
                                                                                                B. thuringiensis delta endotoxin Cry3Bb1v11231 expression cassette #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified polynuclectide useful for controlling Coleopteran insect infestation in a field of crop plants encodes insecticidal crystal 3 Bacillus thuringiensis delta-endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                          /cons_splice= (5'site:NO,3'site:NO)
/note= "Zea mays HSP70 intron"
                                                                                                                                                                                                                                                                                                                                      /*tag= a
/note= "Enhanced CaMV35S promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Cry3Bb1v11231"
3475. .3730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 105-110; 107pp; English
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MONS ) MONSANTO TECHNOLOGY LLC.
 BP.
ABX95186 standard; DNA; 3754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1490. .3451
                                                                                                                                                                                                                                                                                                                                                                        .1472
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/number= 1
                                                                  (first entry)
                                                                                                                                                                                                                                    Agrobacterium tumefaciens.
Cauliflower mosaic virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            '*tag≃
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                      Bacillus thuringiensis.
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/*tag= a /product= "B thuringiensis cry1Bb variant protein"

MONSANTO TECHNOLOGY LLC

(SNOW)

(BOGD/) BOGDANOVA N N. (ROMA/) ROMANO C P.

29-AUG-2002; 2002US-0407428P.

2003WO-US026510

26-AUG-2003;

11-MAR-2004

Location/Qualifiers

Bacillus thuringiensis.

Synthetic.

Key

1241. .4933 /*tag= a

WO2004020636-A1

ds.

insecticidal protein, plant; pesticide; gene therapy; lepidopteran insect pest; transgenic plant; insect infestation resistance; monocot; dicot; crylBb;

expression cassette DNA SeqID11

thuringiensis crylBb-related

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delta-endotoxin relative to the highest levels obtained using prior compositions. In particular, transgenic maize expressing higher levels of the CryBb protein designed to exhibit increased toxicity toward Coleopteran pests deliver superior levels of insect protection and are less likely to sponsor development of populations of target insects that are resistant to the insecticidally active protein. Improved control of susceptible target insect pests and season long protection from insect pathogens is achieved using the modified polynucleotide. The modified polynucleotide reduces the number of transgenic events that have to be screened in order to identify one which contains beneficial levels of one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235
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                                                                                                                                                                                                                                                                                                ore insect controlling compositions. The present sequence represents llus thuringiensis delta endotoxin Cry3Bblv11231 expression cassette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3754;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.3%; Score 554; DB 10;
.larity 94.5%; Pred. No. 6.7e-172;
Conservative 0; Mismatches 30;
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This invention relates to a novel polynucleotide sequence optimised for expression of an insecticidal protein in a plant. The invention may be useful for the production of pesticides whilst the disclosed sequences may be used for gene therapy. The polynucleotide sequence and methods are useful in the control of lepidopteran insect pests, and for producing transgenic plants with the ability to resist insect infestations. The invention provides polynucleotide sequences with enhanced, improved and optimised expression in monocot and dicot plant species. The present sequence is that of a B thuringiensis crylBb expression cassette which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide sequence optimized for expression of an insecticidal protein in a plant, useful in the control of Lepidoptera insect pests, and for producing transgenic plants with the ability to resist insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5170 BP; 1089 A; 1761 C; 1339 G; 981 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5170;
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P-PSDB; ADK98489.
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BP.

ADK98488

ADK98488

ADK98488
ID ADK9
XX
AC ADK9
XX
DT 03-J

(first entry)

03-JUN-2004

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This invention relates to a novel polynucleotide sequence optimised for expression of an insecticidal protein in a plant. The invention may be useful for the production of pesticides whilst the disclosed sequences may be used for gene therapy. The polynucleotide sequence and methods are useful in the control of lepidopteran insect pests, and for producing transgenic plants with the ability to resist insect infestations. The invention provides polynucleotide sequences with enhanced, improved and optimised expression in monocot and dicot plant species. The present sequence is that of a B thuringiensis crylBb expression cassette which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
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                                                                                                                                                                 Length 5600;
                                                                                                                                                                                          Indels
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                                                                                                                                                                 Score 554; DB 12;
Pred. No. 8.2e-172;
0; Mismatches 30;
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Best Local Similarity 94.5%;
Matches 586; Conservative C
                                                                                                                  related to the invention.
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                                    GAAGGTGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
                                                                                                                                                                         GACGITCCAACCACGICITCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                                                                                                                                                                         "B thuringiensis crylBb variant protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           thuringiensis crylBb-related expression cassette DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insecticidal protein; plant; pesticide; gene therapy;
lepidopteran insect pest; transgenic plant;
insect infestation resistance; monocot; dicot; crylBb;
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BOGDANOVA N N.
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P-PSDB; ADK98491.
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Sequence Seq

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Sequence Sequence Sequence

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Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

Searched:

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20 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: DO BOX 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,998A
FILING DATE: 23-FEB-1998
CLESSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.3%; Score 554; DB 3; L
ilarity 94.5%; Pred. No. 7.8e-178;
Conservative 0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/09027998A
Patent No. 6284949
GENERAL INFORMATION:
APPLICANT: Fischhoff, David A
APPLICANT: Prischhoff, David A
APPLICANT: Prisc
US-09-643-971-10
US-09-377-466B-13
US-09-810-861B-3
US-09-810-861B-4
US-09-186-002-15
US-08-038-768A-1
US-08-038-768A-1
US-09-011-151-8
US-09-011-151-8
US-09-737-698B-30
US-09-737-656A-30
US-09-737-658B-29
US-09-737-658B-29
US-09-737-658B-29
US-09-737-626A-29
US-09-737-626A-29
US-09-737-626A-29
US-09-623-551-17
US-08-446-486-31
US-08-446-486-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 661 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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6617.031 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/RECTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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(c) 1993 - 2005 Compugen Ltd.
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Patent No. 6448476;
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.;
TITLE OF INVENTION: Phosphonate Metabolizing Plants;
FILE REFERENCE: 38-21(15303);
CURRENT APPLICATION NUMBER: US/09/441,340;
CURRENT FILING DATE: 1999-11-16;
EARLIER APPLICATION NUMBER: 60/108,763;
NUMBER OF SEQ ID NOS: 32;
SOFTWARE: Patentin Ver. 2.0;
                                                                                                                                                                             30;
                                                                                                                                          Score 554; DB 3; I
Pred. No. 1.5e-177;
0; Mismatches 30;
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Matches 586; Conservative
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LOCATION: (1869)..(2102)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCORMATION:
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants;
ITILE OF INVENTION: Phosphonate Metabolizing Plants;
FILE REFERENCE: 38-21(15303);
CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
ERALIER APPLICATION NUMBER: 60/108,763
ERALIER PLING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                    OTHER INFORMATION: Description of Artificial Sequence: expression OTHER INFORMATION: cassette comprising plant promoter linked to OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked OTHER INFORMATION: to termination sequence FEATURE:
NAME/KEY: promoter
LOCATION: (6)..(620)
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (645)..(715)
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94.5%; Pred. No. 1.5e-177;
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TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 586; Conservative
                                                                                                                                                                                                                                                transit_peptide (1179)..(1406)
                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1407)..(1838)
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LOCATION: (1849)..(2082)
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(729)..(1178)
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US-09-441-340-25
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LOCATION:
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FEATURE:
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TITLE OF INVENTION: Phosphonate Metabolizing Plants FILE REFERENCE: 38-21(15303)

CURRENT APPLICATION NUMBER: US/09/441,340

CURRENT APPLICATION NUMBER: 06/108,763

EARLIER APPLICATION NUMBER: 60/108,763

EARLIER FILING DATE: 1998-11-17

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 31
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Pred. No. 1.6e-177;
0; Mismatches 30;
                                                                                                                                                                                                US-09-441-340-31; Sequence 31, Application US/09441340; Patent No. 6448476; GENERAL INFORMATION:
TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 94.5%;
Matches 586; Conservative
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; NAME/KEY: terminator
US-09-441-340-31
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296 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGAGGTTCCAACCACGTCTTCAA 355
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Sequence 15, Application US/09377466B

Sequence 15, Application US/09377466B

Sequence 15, Application US/09377466B

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Incorrect CURRENT BPLICATION NUMBER: US/09/377,466B

CURRENT APPLICATION NUMBER: US/09/377,466B

NUMBER OF SEQ ID NOS: 43

NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                            388 GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
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                                     208 ATGGACCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA
                                                                                 356 AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
                                                                                                                           268 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTTCAACAAGGGTAATATCCGGA
                                                                                                                                                                     412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                                                                                                                                                                                      532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGTATCTCCACTGACGTAAGG
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LOCATION: (1490)..(3448)
OTHER INFORMATION: Cry3Bbl variant v11231
NAME/KEY: terminator
LOCATION: (3475)..(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
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LOCATION: (25)..(640)
OTHER INFORMATION: P-CaMV.35S
NAME/KEY: intron
LOCATION: (669)..(1472)
OTHER INFORMATION: 1-Zm.Hsp70
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OTHER INFORMATION: Description
OTHER INFORMATION: cassette
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SEQ ID NO 15
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TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILE REFERENCE: 38-21 [15304] Cry3Bb Improved Exp. Corn CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
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                                                                                                         GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
                                                                                                                                                                                                                                                  GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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                                                                                                                                                                GACGITCCAACCACGICITCAAAGCAAGIGGAITGAIGIGAIAICICCACIGACGIAAGG
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OTHER INFORMATION: Cry3Bbl variant 11231mv2
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; Patent No. 6501009
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   CATTIGGAGAGGACACGCIG 731
                                                                                                                                                                                                                                                                                                                                                              CATTTGGAGAGGACACGCTG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: promoter LOCATION: (25)..(640) OTHER INPORMATION: P-CaMV.35S NAME/KEY: 5'UTR LOCATION: (664)..(734) OTHER INFORMATION: L-Ta.hcb1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3217)..(3450)
OTHER INFORMATION: T-Ta.hsp17
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OTHER INFORMATION: I-OS.Act1
NAME/KEY: CDS
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Matches 586; Conservative
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3284 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 3343
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                                                                                    3044 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 3103
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    30; Indels
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Sequence 1, Application US/09434039A

Patent No. 65316A0:
GENERAL INFORMATION:
APPLICANT: MANNERLOEF, Marie
APPLICANT: TENNING, Paul Peter
APPLICANT: TENNING, Per
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 09/434,039A
CURRENT FILING DATE: 1999-11-04
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/112,003
PRIOR APPLICATION NUMBER: 09/182,117
PRIOR APPLICATION NUMBER: 09/182,117
PRIOR APPLICATION NUMBER: 09/182,117
PRIOR APPLICATION NUMBER: 09/182,117
SEQ ID NO 1

LENGWARE: PatentIn version 3.0
SEQ ID NO 1
LENGER: PATENING DATE: 1998-10-29
SOFTWARE: PATENT NO NUMBER: 09/182,117
PRIOR APPLICATION NUMBER: 09/182,117
PRIOR PRIOR APPLICATION NUMBER: 09/182,117
    Mismatches
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94.5%;
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Best Local Similarity
  Matches 586;
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US-09-434-039A-1
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                                                                                                                                                 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCCAAAG
                                                                                                                                                                                                                                     ATGGACCCCCACCCACGAGGACATCGTGGAAAAAGAAGAAGGACGTTCCAACCACCACCTTCAA
                                                                                                                                                                                                                                                                                         AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA
                                           ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCCACAGTGGTCCCAAAG
                                                                                                                                                                                                           ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAAAAGAGCGTTCCAACCACGTCTTCAA
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NUMBER OF SEQUENCES: 27

OMPUTER READABLE PORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/182,117
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Patent No. 6204436
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8012 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity
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2107 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAA 2166
                                                                                                                             1927 ATCATTGCCATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCCAAAG
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                                    116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGGAAACCTCCTCGGATTCCATTGCC
                                                                    1807 rccgarcricaccaracaaagggraararccggaaaccrccrcggarrccarrgcc
                                                                                                         ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                   ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
FILING DATE:
 30;
 Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5, Application US/09182117; Patent No. 6204436; GENBRAL INFORMATION: APPLICANT:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 8418 base pairs
 Conservative
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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                               116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
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APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Method for Transforming Plants
TITLE OF INVENTION: delta-Endotoxins
FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
CURRENT APPLICATION NUMBER: US/09/186,002B
NUMBER OF SEQ ID NOS: 18
SOFTHARE: Patentin Ver. 2.0
 30; Indels
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Pred. No. 3.3e-177;
Mismatches
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CATION: (3666).. (5573)
COTHER INFORMATION: completely synthesized
MS-09-186-002-16
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94.5%;
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ORGANISM: Artificial Sequence
586; Conservative
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LENGTH: 8349
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US-09-186-002-16
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                                        Length 8418;
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                                      Score 554; DB 4; I
Pred. No. 3.4e-177;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09182117; Patent No. 6204436; GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                      Query Match
Best Local Similarity
Matches 586; Conserv
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   US-09-434-039A-5
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US-09-182-117-4
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                                                                         Gaps
                                                                         4,
                                      Length 8418;
                                                                   0; Mismatches 30; Indels
                                  Score 554; DB 3; I
Pred. No. 3.4e-177;
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APPLICANT: TENNING, Paul Peter
APPLICANT: TENNING, Paul Peter
APPLICANT: TERNING, Paul Peter
APPLICANT: TERNING, Paul Peter
APPLICANT: TEREN, Per
CURRENT TELICATION WUMBER: US/09/434,039A
CURRENT FILING DATE: 1999-11-04
PRIOR PILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 8418
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                                  75.3%;
94.5%;
                                  Query Match 75.3
Best Local Similarity 94.5
Matches 586; Conservative
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ORGANISM: Sugar beet
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US-09-434-039A-5
US-09-182-117-5
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3313 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 3372
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                                                                                                                                                                                              3133 TCCGATGTGAGACTTTTCCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                        ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA
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                                                                                                                                           Gaps
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US-096-163-46
Sequence 46, Application US/07936163
Septicant: NOTOHENS ROBERT A
APPLICANT: MERLO, DONALD J
APPLICANT: MERLO, DONALD J
APPLICANT: MERLO, DONALD J
APPLICANT: NOTOHENS ROBERT A
APPLICANT: ORR, GERGORY L
ITILE OF INVENTION: INSECTICIDAL PROTEINS AND METHOD FOR TITLE OF INVENTION: PLANT PROTECTION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSE: THOMAS D. ZINDRICK
STREET: 9002 PURDUE ROAD
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                           4;
                                                                                                         Length 8798;
                                                                                                                                         Indels
                                                                                                                                           30;
                                                                                                       75.3%; Score 554; DB 4; L
94.5%; Pred. No. 3.4e-177;
iive 0; Mismatches 30;
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                                                                                                                                         Matches 586; Conservative
                         LENGTH: 8798
TYPE: DNA
ORGANISM: Sugar beet
                                                                                                                      Best Local Similarity
                                                                          US-09-434-039A-4
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                                                                                                                                           Gaps
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                                                                                                       Length 8798;
                                                                                                                                       30; Indels
                                                                                                       Score 554; DB 3; I
Pred. No. 3.4e-177;
0; Mismatches 30;
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Petent No. 6531649
GENERAL INFORMATION:
APPLICANT: MANURELOEF, Marie
APPLICANT: STEEN, Per
APPLICANT: STEEN, Per
TILE OF INVENTION: Transgenic Plants
FILE REPERENCE: 09/434,039
CURRENT FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/112,003
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 36
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTIN VETSION 3.0
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                       (genomic)
                                                                                                       75.3%;
94.5%;
                                                                                                  Query Match
Best Local Similarity 94.5
Matches 586; Conservative
TOPOLOGY: linear MOLECULE TYPE: DNA (9 HYPOTHETICAL: NO ANTI-SPACE
                                                    ANTI-SENSE: NO
      ; TOPOLOGY:
; MOLECULE TYI
; HYPOTHETICAI
; ANTI-SENSE:
US-09-182-117-4
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US-09-434-039A-4
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Query Match
Best Local Similarity 93.2%;
Matches 588; Conservative
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                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 800
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   RESULT 15
US-08-729-601A-43
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                                                                                                                                                                                                                                                                                                                                                    Length 1030;
                                                                                                                                                                                                                                                                                                                                                                               Indels
ZIP: 46268-1189
COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,163
FILING DATE: 27-AUG-1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                   Query Match
74.9%; Score 551.4; DB 1;
Best Local Similarity 93.2%; Pred. No. 7.7e-177;
Matches 588; Conservative 0; Mismatches 41;
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                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ZINDRICK, THOWAS D
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: C-38,424A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-1869
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 BASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                          linear
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TOPOLOGY:
US-07-936-163-46
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                                                                    APPLICANT: Merlo, Donald J.
APPLICANT: Merlo, Donald J.
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: Modified Bacillus Thuringiensis
TITLE OF INVENTION: Lepidopteran Control in Plants
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle St.
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,601A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 551.4; DB 3;
Pred. No. 7.7e-177;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F.
35,234
60089
Sequence 43, Application US/08729601A, Patent No. 6166302, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Krueger, James P.
REGISTRATION NUMBER: 35,234
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
TELEPHAX: 312-372-7848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1030 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
WOLECULE TYPE: DNA (genomic)
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Search completed: October 11, 2005, 14:58:23 Job time : 186 secs

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October 11, 2005, 12:54:20 ; Search time 718 Seconds (without alignments) 7139.448 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_puBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         nucleic search, using sw model
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length: 2000000000
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736
                             Copyright
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Perfect score:
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Maximum DB
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SUMMARIES

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Sequence 1, Appli
Sequence 3, Appli
Sequence 29, Appl
Sequence 29, Appl
Sequence 25, Appl
Sequence 31, Appl
Sequence 31, Appl
         Description
                         2 US-10-075-105C-1
2 US-10-075-105C-3
US-09-943-692-33
5 US-10-213-791-29
5 US-10-213-791-25
5 US-10-213-791-31
5 US-10-232-665-23
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1360
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2107
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2436
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Match 1
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81.2
75.3
75.3
75.3
75.3
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597.4
          Score
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Result
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NO -004 m	13, Appli 9, Appli 10, Appli 13, Appli 3, Appli 4, Appli 4, Appli 10, Appli		s, Appli 97, Appl 92, Appl 3, Appli 92, Appl 89, Appl 89, Appl	1, Appli 89, Appl 89, Appl 95, Appl 95, Appl
Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 1 Sequence 1		Sequence 2 Sequence 5 Sequence 5 Sequence 9 Sequence 2 Sequence 2 Sequence 9	Sequence 9 Sequence 9 Sequence 9 Sequence 3 Sequence 8 Sequence 8 Sequence 8	
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US-10-232-665- US-10-198-478 US-10-378-810- US-10-759-602- US-10-198-478 US-10-198-478	US-10 198-478 US-10 759-602 US-10 759-602 US-10 759-602 US-10 232-665- US-10 10 792-491 US-10 792-491 US-10 792-491 US-10 792-491	10-322-656 10-473-945 10-473-945 10-161-403 10-161-408 11-006-076	-161-408 -006-076 -161-403 -161-408 -006-076 -161-403	US-10-161-408 US-11-006-076 US-11-006-076 US-10-161-403 US-10-161-403
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ALIGNMENTS

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Sequence 1, Application US/10075105C
Publication No. US20050188432A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
GENERAL INTERFERENCE: 7270-72978
FILE REFERENCE: 7270-72978
FILE REFERENCE: 7270-72978
FILE REFERENCE: 2002-02-13
FRIOR APPLICATION NUMBER: 60/268,358
FRIOR FILING DATE: 2001-02-13
FRIOR FILING DATE: 2001-02-13
FRIOR FILING DATE: 2001-02-13
SEQ ID NO: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO: 18
LENGTH: 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 736;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: CaMV 35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
, OTHER INFORMATION:
US-10-075-105C-1
RESULT 1
US-10-075-105C-1
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1 GGATCCAGCGTGTCCTCCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCG

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APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FISCHHOFF, ROY L.
APPLICANT: FUCHS, ROY L.
APPLICANT: FUCHS, ROY L.
APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBEL: 195--1
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patent In version 3.1
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1181
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                                                                                                                                                                                                                                                                                                                                                                        942 CCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACG 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Recombinant Cauliflower Mosaic Viral Promoter (CaMV35S)
US-09-943-692-33
                                                                                                                                                                                                                822 CATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAAGGTGGCCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA
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                                         DB 22; Length 1360;
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                                     Score 597.4; DB 22
Pred. No. 2.2e-191;
0; Mismatches 1;
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; Patent No. US20020152496A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                     Query Match
Best Local Similarity 99.8%;
Matches 598; Conservative
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   JS-10-075-105C-3
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DEPLICATION NO. US20050188432A1

SGUENCE 3, Application US/10075105C

Publication No. US20050188432A1

SGENERAL INFORMATION:

APPLICANT: Li, Zhijian T

TITLE OF INVENTION: Transgene Expression in Bukaryotes

FILE REFERENCE: 7270-72978

CURRENT FILING DATE: 2002-02-13

PRIOR PELICATION NUMBER: 60/268,358

PRIOR FILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 18
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                                                                                                                                     TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCCAAAGATGGA 300
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GGATCCAGCGTGTCCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCG 60
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                                     AAGGATAGTGGGATTGTGCGTCATCCCTTACGTCAGTGGAGATACTGCAGAAGCTTCTGC
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 OTHER INFORMATION: acetyltransferase, and termination sequence
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Pred. No. 1.4e-176;
0; Mismatches 30;
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; Sequence 25, Application US/10213791
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OTHER INFORMATION: Description of Artificial Sequence:expression
OTHER INFORMATION: cassette comprising plant operable promoter linked
OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA
                                4;
  Length 661
Score 554; DB 9; Length 66
Pred. No. 8e-177;
0; Mismatches 30; Indels
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TITLE OF INVENTION: Phosphonate Metabolizing Pla
TITLE OF INVENTION: Phosphonate Metabolizing Pla
FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/10/213,791
CURRENT FILING DATE: 2002-08-07
PRIOR PLILNG DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATCHTIN VET: 2.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/10213791 Publication No. US20030106096A1 GENERAL INFORMATION:
 75.3%;
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                Similarity 94.5
16; Conservative
              Best Local Simi
Matches 586;
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Pred. No. 1.4e-176;
0; Mismatches 30; Indels
Publication No. US20030106096A1
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants
FILE OF INVENTION: Phosphonate Metabolizing Plants
CURRENT APPLICATION NUMBER: US/10/213,791
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US/09/441,340
PRIOR FILING DATE: 1999-11-16
PRIOR PELICATION NUMBER: 60/108,763
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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al Similarity 94.5%;
586; Conservative
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; LOCATION: (1849)..(2082)
US-10-213-791-25
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LOCATION: (1407)..(1838)
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Best Local Similarity
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LENGTH: 2122
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/10213791
Sequence 31, Application US/10213791
Publication No. US20030106096A1
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants
FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/10/213,791
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US/09/441,340
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VOR. 2.0
SEQ ID NOS: 24
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94.5%; Pred. No. 1.5e-176;
live 0; Mismatches 30;
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| LOCATION: (1498)..(1725)
| FEATURE:
| NAME/KEY: CDS
| LOCATION: (1726)..(2157)
| FEATURE:
| NAME/KEY: terminator
| LOCATION: (2172)..(2427)
| US-10-213-791-31
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Best Local Similarity 94.5
Matches 586, Conservative
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LOCATION: (670)..(1473)
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NAME/KEY: promoter
LOCATION: (26)..(64
FEATURE:
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APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/10/232,665
CURRENT FILING DATE: 2002-08-29
PRIOR PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 3754
TYPE: DNA
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                                                                                                                                   Length 3469;
                                                                                                                                   75.3%; Score 554; DB 15;
llarity 94.5%; Pred. No. 1.9e-176;
Conservative 0; Mismatches 30;
OTHER INFORMATION: Cry3Bb1 variant 11231mv2 FEATURE:
NAME-KEY: terminator
LOCATION: (3217)..(3450)
OTHER INFORMATION: T-Ta.hsp17
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Matches 586; Conserv
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; Bublication No. US20030115630A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; TITLE OF INVENTION UNMERS: US/10/232,665
; CURRENT PELING DATE: 2002-08-29
; PRIOR PILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PATENTIN Ver. 2.0
; SOFTWARE: PATENTIN Ver. 2.0
                                                                              296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355
                                                                                                   208 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGAGGTTCCAACCACGTCTTCAA 267
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    236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
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OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
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OTHER INFORMATION: P-CAMV.35S
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LOCATION: (748)..(1238)
OTHER INFORMATION: I-OS.Actl
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OTHER INFORMATION: L-Ta.hcb1
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LOCATION: (1241)..(3199)
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NAME/KEY: promoter
LOCATION: (25)..(6
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NAME/KEY: 5'UTR
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                                                                                                                                                                                                                                                                                                                                                                                                    CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAAGGTGGCTCCTACAAATGCC
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                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                    LOCATION: (3475)...(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
                        OTHER INFORMATION: Description of Artificial Sequence: expression OTHER INFORMATION: cassette
                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                  Length 3754;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                75.3%; Score 554; DB 15;
larity 94.5%; Pred. No. 1.9e-176;
Conservative 0; Mismatches 30;
                                                                                                                                                                                   variant v11231
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                                               FEATURE:
NOCATION: (25)...(640)
OTHER INFORMATION: P-CaMV.35S
ORGANISM: Artificial Sequence
                                                                                                                      ION: (669)..(1472)
INFORMATION: I-Zm.Hsp70
                                                                                                                                            FEATURE:
NAME/KEY: COSS
LOCATION: (1490). (3448)
OTHER INFORMATION: Cry3Bbl vi
FEATURE:
NAME/KEY: terminator
LOCATION: (3475). (3730)
                                                                                                                                                                                                                                                                                           al Similarity
586; Conserv
                                                                                                            NAME/KEY: intron
                                                                                                                                                                                                                                                ; OTHER INFORM
US-10-232-665-15
                                                                                                                      LOCATION:
OTHER INFO
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Matches 58
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, RESULT

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APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxy; FITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxy; FILE REFRENCE: 38-21 (13447) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/186, 002
PRIOR PILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 8349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1807 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 CAGCTATCTGTCACTTCAAAAGGACAGTAGAAAAGGAAAGGTGGCACCTACAAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2047 AGCAAGTGGATTGATGTGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 554; DB 16;
Pred. No. 2.9e-176;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: completely synthesized
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Sequence 16, Application US/10198478
Publication No. US20030188336A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTTGGAGAGACACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: artificial sequence
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Best Local Similarity 94.5%;
Matches 586; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (1). (8349)
CTHER INFORMATION:
US-10-198-478-16
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JS-10-759-602-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3550 crigcagarcrecardegregagacrirricaacaaagegraararccegaaaccreceg 3491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 ATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACA 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 CAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCGTG 582
                                                                         APPLICATT: Rubin-Wilson, Beth
APPLICATT: Rubin-Wilson, Beth
APPLICATT: Smith, Kelley A
TITLE OF INVENTION: PROMOTER AND INTRON FROM MAIZE ACTIN DEPOLYMERIZING
TITLE OF INVENTION: FACTOR
FILE REPERENCE: 50655
CURRENT APPLICATION NUMBER: US/10/378,810
CURRENT APPLICATION NUMBER: US 60/167,111
PRIOR PILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 5796
                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 CTGCAGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Length 5796;
                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:pDAB305
US-10-378-810-2
                                                                                                                                                                                                                                                                                                                                                                                            Score 551.4; DB 17; Length
Pred. No. 1.8e-175;
0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2950 AGTICATITICATITIGGAGAGACACGGGGGA 2920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTICATITICATITIGAGAGGACACGCTGGA 733
                              Sequence 2, Application US/10378810 Publication No. US20030213009A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.2%;
Matches 588; Conservative
RESULT 10
US-10-378-810-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165
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                                                                                                                                                                                                                                                                                                       Moosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.9%; Score 551.4; DB 19; Length 5897; Best Local Similarity 93.2%; Pred. No. 1.9e-175; Matches 588; Conservative 0; Mismatches 41; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/759,602
RILING DATE: 16-Jan-2004
CLASSIFICATION: «UDKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-759-602-26
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DowAgroSciences LLC
Sequence 26, Application US/10759602
Publication No. US20040143868A1
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
Menke, Michael A
Pareddy, Dayakar
Petolino, Joseph F.
Smith, Kelley
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 5110
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                     GTAGAAAAGGAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTT
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TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/759,602
FILING DATE: 16-Jan-2004
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                             AGTICATITICATITIGAGAGACACGCIGGA 733
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DowAgroSciences LLC
STREET: 9330 Zionsville Road
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ainley, Michael
Armstrong, Katherine
Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph F.
Smith, Kelley
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       %Sequence 19, Application US/10759602; Sequence 19, Application US/10759602; Publication No. US20040143868A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 317 337 5110
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 19:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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LENGTH: 9335 base pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Indiana
COUNTRY: USA
ZIP: 46268
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APPLICANT: Corbin, David R.
APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxy;
FILE REFERENCE: 38-21 (13547) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
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                                                                                                                                                                                                   226 TACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGT
                                                                                                                                                                                                                                                                                                                                    1972 TACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGT
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                                                                                                    TGCAGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGA
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                                                        Gaps
                                                      5
  Length 9335;
                                                   Indels
     DB 19;
                                                        41;
  Score 550.4; DB 19
Pred. No. 5.1e-175;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5452 GTTCATTTCATTTGGAGAGAACACGGGGGA 5481
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  74.8%;
93.2%;
Query Match
Best Local Similarity 93.2
Matches 587; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: NAME/KEY: misc_feature
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                                                                                                                               FEATURE:
OTHER INFORMATION: completely synthesized
FEATURE:
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| NAMYKEY: misc feature
| LOCATION: (3660) ..(3773)
| OTHER INFORMATION: "n" = g, a,
| FEATURE:
| NAMEKEY: misc feature
| LOCATION: (4355) ..(4407)
| OTHER INFORMATION: "n" = g, a,
| US-10-198-478-15
   PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
                                                                                             TYPE: DNA ORGANISM: artificial sequence
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                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (1). (10312)
OTHER INFORMATION:
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Best Local Similarity
                                                         SEQ ID NO 15
LENGTH: 10312
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APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox FILE REFERENCE: 38-21 (1354) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/186, 002
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74.7%; Score 550; DB 16; Length 10249;
Best Local Similarity 94.5%; Pred. No. 7.3e-175;
Matches 582; Conservative 0; Mismatches 30; Indels 4;
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                                | FEATURE: | NAME/KEY: misc feature | NAME/KEY: misc feature | LOCATION: (3597) .. (3670) | FEATURE: | NFORWATION: """ = 9, | NAME/KEY: misc feature | LOCATION: (4292) .. (4344) | CHER INFORMATION: """ = 9, | US-10-198-478-14
LOCATION: (1)..(10249)
OTHER INFORMATION:
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                                                          APPLICANT: Corbin, David R.
APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox FILE REPERBNCE: 38-21 (13347) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR PILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 13
LENGTH: 10339
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94.5%; Pred. No. 7.3e-175;
Live 0; Mismatches 30;
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NAME/KEY: misc_feature
LOCATION: (1)..(10339)
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3687)..(3760)
OTHER INFORMATION: "n" = g, a, c, or
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4382)..(4434)
OTHER INFORMATION: "n" = g, a, c, or
US-10-198-478-13
; Sequence 13, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: artificial sequence
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Matches 582; Conservative
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b 559 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 718

c 612 CATTGGAGAGGACAC 727

b 619 CATTTGGAGAGGACAC 634
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Search completed: October 11, 2005, 15:38:12 Job time : 722 secs Н

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CG472761 GQ0081.BR
CK437924 GQ0081.BR
CK437920 GQ0081.BR
CK437836 GQ0081.BR
CK438485 GQ0085.BR
CK438485 GQ0085.BR
CK438486 GQ0085.BR
CK43848 GQ0085.BR
CK43848 GQ0085.BR
CK43848 GQ0085.BR
CCA38115 MGXb00037
CG88115 MGXb00037
CG8819 1118056A0
BZ581291 3590.1.18
BZ586494 31590.1.18
BZ586494 31590.1.23
CG805917 1118056D1
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CG805017 1118056D1
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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BZ590353 BZ5890353 BZ5899055 BBZ586953 BBZ586955 BBZ586955 BBZ586952 BBZ586952 BBZ586952 BBZ586952 BBZ586952 BBZ586952 BBZ586952 BBZ586953 CG709945 CG709523 CG709523 BBSS8533 CG709523	ALIGNMENT: 1983 19.8R_M18 GQ008: Cambium_phla 1983.1 GI:40769778 19 Glauca (white spruce) 10 Gobb. 11 Good, J., Pavy, N., 11 E., Butterfield, Y., Barber (qui,A., Holt,R., Marra,M. and Can East sequencing in Picea gillished (2004) 10 Gobb. 11 Gobb. 12 Gobb. 13 Glauca (Spreading Mackay 14 Gobb. 15 Granication/Qualifiers 16 Glumn: M. 17 Gobb. 18 Gluma: Mackay 19 Gloues available throw 10 Glones available throw 10 Glones available throw 11 Granism. B column: M. 12 Gobb. 13 Granism. B column: M. 14 Gasistant professor EMAI 16 Gobb. 17 Gobb. 18 Gluma: M. 18 Gloualifiers 19 Golumn: M. 10 Gobb. 10 Glone= "GQ0085 M18" 10 Gobb. 11 Gobb. 12 Gobb. 13 Granism. Pg-653" 14 Garanism. Pg-653" 16 Gluma: M. 17 Granism. Pg-653" 18 Gluma: M. 18 Glone= "GQ0085 M18" 19 Granism. Pg-663" 10 Glone= "GO085 M18" 10 Glone= "GQ0085 M18" 11 Gobb. 11 Gobb. 12 Granism. Pg-653" 13 Glauca. 14 Garanism. Pg-663" 15 Granism. Pg-663" 16 Gluma: M. 17 Granism. Pg-663" 18 Gluma: M. 18 Glone "Gobb. 19 Gluma: M. 10 Glone "Gobb. 10 Glone "Gobb. 10 Glone "Gobb. 11 Gobb. 11 Gobb. 12 Gobb. 13 Glone "Gobb. 14 Granism. Pg-663" 15 Gobb. 16 Glone "Gobb. 17 Glone "Gobb. 18 Glone "Gobb. 18 Glone "Gobb. 19 Glone "Gobb. 10 Glone "Gobb. 10 Glone "Gobb. 11 Glone "Gobb. 11 Glone "Gobb. 11 Glone "Gobb. 12 Glone "Gobb. 13 Glone "Gobb. 14 Glone "Gobb. 15 Glone "Gobb. 16 Glone "Gobb. 17 Glone "Gobb. 18 Glone "Gobb. 18 Glone "Gobb. 18 Glone "Gobb. 19 Glone "Gobb. 10 Glone "Gobb. 11 Glone "Gobb. 11 Glone "Gobb. 11 Glone "Gobb. 12 Glone "Gobb. 13 Glone "Gobb. 14 Glone "Gobb. 15 Glone "Gobb. 16 Glone "Gobb. 17 Glone "Gobb. 18 Glone "Gobb. 18 Glon
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/tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem"
/dev stage="Wascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling
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                        Paule, C., Seguin, A.,
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                                                                                                                                                                                                                                                 Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: MNS197113 Clone ID: GQ0081.BR K09 Clones available through: John MacKay, Ph. D. Professeur adjoint -Assistant professeor EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                                                                                                        (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
                                                                                                                                                                                          Quebec, Quebec, CANADA G1K 7P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="E. coli DH10B cells"
/clone_lib="GQ008: Cambium, phloem and bark of girdled
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1 (bases 1 to 702)
Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., S
Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J.,
Siddiqui, A., Holt, R., Marra, M. and MacKay, J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
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ilarity 94.7%; Pred. No. 1.8e-160;
Conservative 0; Mismatches 29;
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Pavillon Charles Eugene Marchand,
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
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/organism="Picea glauca"
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/strain="pg-653"
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                                                                                                                            Contact: John MacKay
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Picea glauca
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopaida; Coniferales; Pinaceae; Picea.
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GQ0081.BR.1 K09 GQ008: Cambium, phloem and bark of girdl
Picea glauca cDNA clone GQ0081.BR_K09 5', mRNA sequence.
CO472768
    /clone_lib="GQ008: Cambium, phloem and bark of
                                                                                                                                                                                                                                                       Length 698;
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                                                                                                                                                                                                                                                 Score 546.6; DB 7;
Pred. No. 1.8e-160;
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CO472761 803 bp mRNA linear EST 09-JUL-2004 GQ0081.BR.1 G07 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0081.BR_G07 5', mRNA sequence. CC472761.1 GI:S0141306
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Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
/note="Organ: Main stem of 4 year old saplings,
approximately 60 cm tall; Vector: pBluescript II SK (+)
KR, Sitel=1: Eco-RI; Site_2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (In
vitrogen) for propagation"
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Pred. No. 1.9e-160;
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ilarity 94.7%;
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Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN_id Identifier: MNS173701 Clone ID:
0Q0003 H02 Clones available through: John Mackay, Ph. D. Professeur
adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
Plate: 3 row: 02 column: H
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GQ0083.BR H02 GQ008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0083_H02 5', mRNA sequence.
CK438332
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Spermatophyta; Coniferopsida, Coniferales; Pinaceae; Picea.

I (bases I to 755)

Morency, M. -J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)

Contact: John MacKay
Centre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem"
/dev stage="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling
   GACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGGAGGTT 508
                                                                                                                                                                                                                          CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC 568
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Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
Fax: 418 67493
Email: jmackay@rsvs.ulaval.ca
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Cambium, phloem and bark of girdled
                                                          GGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCC
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/mol_type="mRNA"
/strain="pg-653"
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/sex="Hermaphrodite"
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/clone_lib="G0008:
saplings"
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Picea glauca
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/sex="Hermaphrodite"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem"

flow stage="Vascular cambium, secondary phloem, and bark
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                                                                                                                                                                                                                                                                                                Forestiere
                                                                                                                        Universite Laval

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Fax: 418 656 749

Email: jmackay@rsvs.ulaval.ca

Email: jmackay@rsvs.ulaval.ca

Center for Computational Genomics and Bioinformatics (CCGB),

University of Minnesota, Mw id Identifier: MNS198052 Clone ID:

GQ0081.BR G07 Clones available through: John MacKay, Ph. D.

Professeur adjoint -Assistant professor EMAIL:

Jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere

(Rorest Biology Research Center) Universite Laval Quebec, Quebec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="GQ008: Cambium, phloem and bark of girdled saplings"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT
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Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J., Siddiqui,A., Holt,R., Marra,M. and MacKay,J. Arborea EST sequencing in Picea glauca (white spruce) Unpublished (2004)
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                                                                                      Contact: John MacKay
Centre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. coli DH10B cells'
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0081.BR G07"
/sex="Hermaphrodice"
                                                                                                                                                                                                                                                                                                                                                           row: 07 column: G
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Seg primer: M13 Reverse
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Control of Recherchay
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Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Control of Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5171860 Clone ID:
GQ0081 K09 Clones available through: John MacKay, Ph. D. Professeur
adjoint Assistant professor EMAIL: jmackay@srsvs.ulaval.ca
center biologie Porestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
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/dev stage="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 713)
Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Morency,M.-J., Eatherfield,Y., Barber,S., Yang,G., Stott,J., Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
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GQ0081.BR K09 GQ008: Cambiuu, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0081_K09 5', mRNA sequence.
CK437984
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/clone_lib="GQ008: Cambium, phloem and bark of girdled
GGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCC
                                                                   391 GGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC
                                                                                                                                                  GACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAAAGAAGACGTT
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days after girdling
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/mol_type="mRNA"
/strain="pg-653"
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Seg primer: M13 Reverse Primer.
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/clone="GQ0081_K09"
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Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 741)
XR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (In vitrogen) for propagation"
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GQ0083.BR J24 GQ008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0083_J24 5', mRNA sequence.
CK438362
                                                                                                                                                                      121 AGTGAGACTTTTCAACAAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT
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                                                                                                                                            Gaps
                                                                                                                Length 713;
                                                                                                                                            Indels
                                                                                                               Score 544.6; DB 7;
Pred. No. 7.8e-160;
0; Mismatches 31;
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Picea glauca
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Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: MN5173771 Clone ID: GQ0083_J24 Clones available—through: John MacKay, Ph. D. Professeur adjoint—Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA GIK 7P4 Seq primer: M13 Reverse Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Approximately 60 cm tall; Vector: pBluescript II SK (+) XR; Site 1: Eco-RI; Site 2: Xho-II, Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (In
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                                                                                                                     Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4 Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
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/sex="Hermaphrodite"
/sex="Hermaphrodite"
/tissue type="Wascular cambium, secondary phloem and of trees girdled by removing a ring of bark ca. 1 cm from the midpoint of the main stem"
/dev stage="Wascular cambium, secondary phloem, and b from trees harvested 1 and 7 days after girdling
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/clone_lib="GQ008: Cambium, phloem and bark of
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llarity 94.4%; Pred. No. 7.9e-160;
Conservative 0; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:3330"
                                                                     en Biologie
  in Picea
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                              Contact: John MacKay
Centre de Recherche
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CK438485 T36 bp mRNA linear EST 08-JAN-2004 GQ0085.BR_M24 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0085_M24 5', mRNA sequence.
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1 (bases 1 to 736)
Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, B., Butterfield, Y., Barber, S., Yang, G., Stott, J., Siddiqui, A., Holt, R., Marra, M. and MacKay, J.
Arborea EST sequencing in Picea glauca (white spruce)
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  XR vector (Stratagene), into DH10B cells (In
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                                                                                                      Score 537.2; DB 7;
Pred. No. 1.6e-157;
into the pBluescript II SK (+) transformed by electroporation vitrogen) for propagation"
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Picea glauca
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                                                                                                      Query Match
Best Local Similarity 92.5%;
Matches 567; Conservative
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/mol_type="mRNA"
/etrain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0081_PO5"
/sex="Hermaphrodite"
/fissue Lype="vascular cambium, secondary phloem and bark
/fissue Lype="vascular cambium, secondary phloem and bark
/fissue Lype="vascular cambium, secondary phloem, and bark
from the midpoint of the main stem
/dev stage="vascular cambium, secondary phloem, and bark
from_trees harvested 1 and 7 days after girdling
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Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5171736 Clone ID:
GQ00081_FOS Clones available Through! John Mackay, Ph. D. Professeur
adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
Center Diversite Laval Quebec, Quebec CANADA GIK 7P4
Plate: 1 row: 05 column: F
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                GQ0081.BR_F05 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0081_F05 5', mRNA sequence.
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1 (bases 1 to 655)
Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Arborea EST sequencing in Picea glauca (white spruce) Unpublished (2004)
Contact: John MacKay
Centre de Recherche en Biologie Forestiere
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                                                                                                                                                                                                                                                         636
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/lab_host="E. coli DH10B cells"
/clone_lib="GQ008: Cambium, phloem and bark of girdled
                                                                                                                                                                                                                                     397 GGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC
                                                                 CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC
                                                                                                                                                       CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCTCACTGACGTAAGGGATGAC
                                                                                                                                                                                                             GCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAAAGGAAGTTCATTTCATTTG
                                         GACAGTGGTCCCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAAAGAAGATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cea glauca (white spruce)
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AUTHORS
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CK437920
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657

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Fax: 418 656 7433

Email: jmackay@revs.ulaval.ca
Conter for Computational Genomics and Bioinformatics (CCGB),
Connersity of Minnesota, NN id Identifier: MNS174387 Clone ID:
GQ0085 D16 Clones available through: John MacKay, Ph. D. Professeur
adjoint Assistant professor EMAIL: jmackay@revs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
Plate: 5 row: 16 column: D
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                     EST 08-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.

Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.

Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Ashorea EST sholt, R., Marra, M. and MacKay, J.

Arborea EST scholt, R., Marra, M. and MacKay, J.

Onpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                          698 bp mRNA linear EST 08-JAN-201 GQ0085.BR D16 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0085_D16 5', mRNA sequence.
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papproximately 60 cm tall, vector: pBluescript II SK (+)
XR, Site_1: ECO-RI; Site_2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH108 cells (In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and bark
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  CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC
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/clome_lib="GQ008: Cambium, phloem and bark of
saplings"
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Centre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 533.2; DB 7;
Pred. No. 3e-156;
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/mol_type="mRNA"
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/clone="GQ0085_D16"
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Picea glauca
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94.5%;
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CK438348
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                                                                                                Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MNS174611 Clone 1D:
University of Minnesota, MN id Identifier: MNS174611 Clone 1D:
adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
Seg primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCCACCACGAGGAGCATCGTGGAAAAAAAGAAGTTCCAACCACGTCTTCAAAGCAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA 300
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approximately 60 cm tall; Vector: pBluescript II SK (+)
RR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (In
vitrogen) for propagation"
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Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
Fax: 418 656 7493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="GQ008: Cambium, phloem and bark of girdled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCT
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Pred. No. 7.1e-157;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment"
/lab host="E. coli DH10B cells"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="taxon:3330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'sex="Hermaphrodite"
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al Similarity 94.8%;
565; Conservative
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                                                                                                                                                    /sex="Hermaphrodite"
/fissue type="Xylem, pith, cambium, phloem, bark"
/dev_stage="Primary & secondary shoot, secondary phloem
pooled from plants fertilized with low and high NH4NO3"
/lab_host="E. coli DH10B cells"
/clone lib="GQ016: Primary, secondary SHOOT -N fertil.
Treatments"
                                                                                                                                                                                                                                                                                     /note="Organ: Main stem region producing secondary gro
on 60 cm tall seedlings; Vector: pBluescript II SK (+)
Site 1: ECO-RI; Site 2: Kho-I; cDNA was prepared from
of poly A+ selected RNA and was directionally ligated
the pBluescript II SK (+) XR vector (Stratagene),
transformed by electropoxation into DH10B cells (In
vitrogen) for propagation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CCTACAAATGCCATCATTGCGATAAAGGAAAAGGCCATCGTTGAAGATGCCTCTGCCGACA
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Pred. No. 9e-140;
0; Mismatches 32;
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                                                                   /organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:330"
/clone="GQ0165_M24"
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Plate: 5 row: 24 column: M
Seq primer: T7 Primer.
Location/Qualifiers
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Best Local Similarity 93.6%;
Matches 510; Conservative
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Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesora, MN id Identifier: MN5268594 Clone ID:
GQ0165_M24 Clones available_through: John MacKay, Ph. D. Professeur
adjoint —Assistant professor EMAIL: jmackayorsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CO481168 610 bp mRNA linear EST 09-JUL-2004 GQ0165.B7 M24 GQ016: Primary, secondary SHOOT -N fertil. Treatments Picea glauca cDNA clone GQ0165_M24 3', mRNA sequence.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.

1 (bases 1 to 610)
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Arborea EST sequencing in Picea glauca (white spruce) Unpublished (2004)
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 Mismatches
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Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Pramework to Sequence the Magnaporthe grisea
                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 839)
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larity 99.4%; Pred. No. 4.1e-99;
Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                             Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 58
High quality sequence stop: 454.
                                                                     Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                cione mgxb0003F18f, genomic survey sequence-
AQ362115
AQ362115.1 GI:4211034
                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Magnaporthe grisea"
                                                                                                                                                                                                                 Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db xref="taxon:148305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="70-15"
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CG206846 154 bp DNA linear GSS 21-AUG-2003 TOS0467 TAMU Rice Japonica Nipponbare BAC Library (Hind III) Oryza sativa (japonica cultivar-group) genomic clone TOSJNBh019I10h,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Branartoideae; Oryzae, Inliopsida; Poales; Poaceae;
I. (bases 1 to 654)
Li, Y., Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.
BAC end sequences to close the gaps of a rice physical map at TAMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGATTGATGTGACATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGACACGCTGGATC 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCCACCTACAATGCCATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="TAMU Rice Japonica Nipponbare BAC Library (Hind III)"
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733
                                         517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db xxef="xxon:39947"
/clone="TOSUNBh019110h"
                      679 CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGACACGCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics and Biotechnology
Texas A & M University
TAMU 2474, College Station, TX 77843-2474, USA
Fel: 979 862 4800
Fax: 979 862 4800
Email: c-wu@neo.tamu.edu
Seg primer: M13 universal Forward GTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
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97.2%; Pred. No. 9.4e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="E. coli DH10B"
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Location/Qualifiers
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                                                                                                                                                                                                                 genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wu C
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Best Local Similarity
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                                                                                                        RESULT 12
CG206846/c
                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                      ACCESSION
VERSION
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AUTHORS
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/done lib="3590 - RescueMu Grid M"
/clone lib="3590 - RescueMu Grid M"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BgJII;
RescueMu is a 4.9 kb; modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamHi and BgIII, and ligated to form circular
plasmids. DH10B cells were transformed and then screened
                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 17-DEC-2002
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      CCCCCACCACGAGGAGCATCGTGGAAAAAAAAGAAGTTCCAACCACCTCTCAAAGCAA 152
                                                                                                   678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize genomic sequences found using engineered RescueMu transposon
                                                                                                                                                       92
                                                                                                                                        151 GTGGATTGATGTGATATCTCCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCG
                                                                                                619 GTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was trimmed. Post-ligation
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                                                                                                                                                                                                                                                                                                                                                                                                         3590_1 83_1 F06.y_1 3590 - RescueMu Grid M Zea mays genomic, genomic survey sequence.
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon.4577"
/tissue_type="leaf"
/lab_host="bH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
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on LB plates with ampicillin.
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Plate: 3590_1_83_1 column: 11

Class: transposon_tagged.
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Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:27226352
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Best Local Similarity 96.15
Matches 341; Conservative
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BZ591291.1
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AUTHORS
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JOURNAL
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/dav stage="leaf"
/dav stag
                                                                                                                                                                                   CG730119 496 bp DNA linear GSS 20-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCTGTCACTTTATCGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCAT 272
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGACACGCTCGATC 168
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/cultivar="mixed background W23/A188/B73/K55"
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Fax: 650 725 8227
Email: walbot@stanford.edu
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Pred. No. 1.2e-93;
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Best Local Similarity 96.3%;
Matches 342; Conservative
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1118056A07.y1 1118 - RescueMu Grid S Zea mays genomic, genomic
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Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 1118056 row: 40
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/mol_type="genomic DNA"
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/lab_host="DH10B"
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Tel: 650 723 2227
Fax: 650 725 8221
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DB 9; Length 469;

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Query Match

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